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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 16:43:55 ; Search time 12994 Seconds
(without alignments)
12072.116 Million cell updates/sec

Title: US-09-715-927-7
Perfect score: 7496
Sequence: 1 agctgctcaggcgctccgc.....gttgagcatggagaaaaaa 7496

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htgo_inv.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

C	1	3113	41.5	167891	9	AC013439	AC013439 Homo sapi
C	2	684.8	9.1	67729	2	AC073035	AC073035 Homo sapi
	3	653	8.7	67729	2	AC073035	AC073035 Homo sapi
	4	647.6	8.6	2222	9	AF226614	AF226614 Homo sapi
	5	647.6	8.6	2824	6	AX188313	AX188313 Sequence
	6	647.6	8.6	3081	6	AX047362	AX047362 Sequence
	7	647.6	8.6	3333	6	AX086462	AX086462 Sequence
	8	647.6	8.6	3333	9	HSB801908	AL136944 Homo sapi
	9	646	8.6	2443	9	AF231121	AF231121 Homo sapi
	10	641.2	8.6	3317	9	AF215636	AF215636 Homo sapi
	11	637.4	8.5	62947	2	AC083764	AC083764 Homo sapi
	12	633.6	8.5	2286	9	AK002038	AK002038 Homo sapi
	13	513	6.8	513	9	AF147322	AF147322 Homo sapi
	14	488.8	6.5	172437	2	AC096437	AC096437 Rattus no
	15	475.8	6.3	1949	10	AF394785	AF394785 Rattus no
	16	460	6.1	2129	10	RRU76714	U76714 Rattus norv
	17	453	6.0	2111	10	AF215637	AF215637 Mus muscu
	18	453	6.0	2130	10	AF226613	AF226613 Mus muscu
	19	453	6.0	3273	10	BC003438	BC003438 Mus muscu
	20	452.6	6.0	3304	10	AF231120	AF231120 Mus muscu
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	22	337	4.5	486	6	AX187577	AX187577 Sequence
	23	337	4.5	527	6	AX184710	AX184710 Sequence
	24	337	4.5	628	6	AX186515	AX186515 Sequence
	25	282	3.8	166526	2	AC079209	AC079209 Homo sapi
	26	279.8	3.7	177720	9	AC019193	AC019193 Homo sapi
C	27	279.8	3.7	183245	2	AC099397	AC099397 Homo sapi
	28	279.4	3.7	158430	2	AC09545	AC09545 Homo sapi
C	29	279.4	3.7	182312	2	AC099056	AC099056 Homo sapi
C	30	278.4	3.7	154792	2	AC108111	AC108111 Homo sapi
	31	278	3.7	44327	9	HSB277557	AL277557 Homo sapi
	32	278	3.7	93713	9	AC006071	AC006071 Homo sapi
C	33	278	3.7	95456	2	AC002092	AC002092 Homo sapi
C	34	277.8	3.7	88484	9	AL355794	AL355794 Human DNA
	35	276.8	3.7	130964	9	AP000609	AP000609 Homo sapi
C	36	276.8	3.7	183085	9	AC005815	AC005815 Homo sapi
C	37	276.6	3.7	157985	9	CNS05TEM	AL163853 Human chr
	38	276.6	3.7	203790	9	AC010422	AC010422 Homo sapi
C	39	276.6	3.7	215849	2	AC007939	AC007939 Homo sapi
	40	276.2	3.7	156100	2	AC011934	AC011934 Homo sapi
	41	276	3.7	12619	6	AX239606	AX239606 Sequence
C	42	276	3.7	185832	9	AL137800	AL137800 Human DNA
C	43	276	3.7	305000	9	HSXDPA	AL590762 Homo sapi
C	44	275.8	3.7	400	11	GL1389	GL1389 SHGC-10164
C	45	275.8	3.7	435	6	AX333915	AX333915 Sequence

ALIGNMENTS

RESULT 1
AC013439/c
LOCUS AC013439 167891 bp DNA linear PRI 07-NOV-2001
DEFINITION Homo sapiens BAC clone Rp11-270G18 from 2, complete sequence.
ACCESSION AC013439
VERSION AC013439.11 GI:13270751
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 167891)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 95063792
REFERENCE 2 (bases 1 to 167891)
AUTHORS Nguyen,C., Cotton,M., Hawkins,M. and Spalding,L.
TITLE The sequence of Homo sapiens BAC clone Rp11-270G18
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 167891)
AUTHORS Waterston,R.H.
TITLE Direct Submission

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JOURNAL Submitted (11-NOV-1999) Genome Sequencing Center, Washington
REFERENCE University School of Medicine, 4444 Forest Park Parkway, St. Louis,
AUTHORS MO 63108, USA
TITLE Waterston,R.
JOURNAL Direct Submission
REFERENCE Submitted (09-AUG-2001) Department of Genetics, Washington
AUTHORS University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
TITLE 5 (bases 1 to 167891)
JOURNAL Waterston,R.
COMMENT Direct Submission
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapient@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0270G18
-----

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanese,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at the Roswell Park Cancer Institute
(http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is AC068833; the clone sequenced to
the right is RP11-88120, 200 bp overlap. Actual start of this
clone is at base position 1 of RP11-270G18; actual end is at base
position 167891 of RP11-270G18.
Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="2"
/map="2"
/clone.lib="RPCI-11"
/clone="RP11-270G18"
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repeat_region 155. 356
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repeat_region 357. 529
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repeat_region 530. 1024
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FEATURES
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1053. 1237
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1289. 1449
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repeat_region
2016. 2795
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repeat_region
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Db 126108 ATGGTGTACAGAACTCCATGAACTATCTTCTGTATCTTCTGCAATTTTCATCATGTCATCC 126049

QY 7116 tggctccaaatcctgaagcttttggcttgcgtatgatttcagttcctcttggcga 7175
|||||

Db 126048 TGGCTCCAAATCCTGAAAGCTTTTGGCTTGGTCGTATTTGATTTTCAGTCTCCTTTTGGCAA 125989
|||||

QY 7176 tgggccaattatgtatttcgcatcttcccaaaatactcggaaacaagctctttgctt 7235
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Db 125988 TGGGCCACATATGATTTTCGATTTCCCAAAATATCTCGGGAACAAGCTCTTGTCTT 125929
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QY 7236 qcggtcctgatgcaaaagaagtttaggaagcaaaatcagaatcacatctgtgtttgag 7295
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Db 125928 GCGGTCTGTATGCAAAAGAGTAGGAGGAAATCAAGCAATACATCTGTTTGTGAG 125869
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QY 7296 acagtttaactgttgcctactctgttactatgattatagagcacatgctgtatttggta 7355
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Db 125868 ACAGTTTAACTGTGCTATCTGTTACTAGATTTATATAGACACATGCTGCTTATTTTGT 125809
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QY 7356 ctgcagaattccaataatggctgggtgttttgcctctgttttttaccacagctgaccttg 7415
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Db 125808 CTGCAGAAATTCCTCAATAATGGCTGGGTGTTTGTCTGCTGTTTACCACAGCTGTGCCCTG 125749
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QY 7416 agaactaaaagctgttttaggaacccttaagtcagcagaaaataactgatttaattccctta 7475
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Db 125748 AGAATAAAAGCTGTTTAGGAAACCTAAGTCAGCAGAAATTAACGTATTAATTCCTTA 125689
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QY 7476 tgttgagcctgggaaaaaaa 7496
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Db 125688 TGTTGAGGCATGGAAAAAAA 125668
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RESULT 2
AC073035/c
LOCUS
DEFINITION Homo sapiens chromosome 2 clone RP11-38301 map 2, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC073035
VERSION AC073035.1 GI:8347978
KEYWORDS HTG; HTGS_PHASE0.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 67729)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Abrahams, H., Allen, N., Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bedalov, F., Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G., Campopiano, A., Castle, A., Choepel, X., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRoque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mieng, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisan, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigliolo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, N.
Direct Submission
Submitted (08-JUN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10434
Center clone name: 383_O_1

* NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1 780: contig of 780 bp in length
* 781 880: gap of 100 bp
* 881 1643: contig of 763 bp in length
* 1644 1743: gap of 100 bp
* 1744 2514: contig of 771 bp in length
* 2515 2614: gap of 100 bp
* 2615 3382: contig of 768 bp in length
* 3383 3482: gap of 100 bp
* 3483 4258: contig of 776 bp in length
* 4259 4358: gap of 100 bp
* 4359 5117: contig of 759 bp in length
* 5118 5217: gap of 100 bp
* 5218 6007: contig of 790 bp in length
* 6008 6107: gap of 100 bp
* 6108 6875: contig of 768 bp in length
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* 7842 8623: contig of 782 bp in length
* 8624 8723: gap of 100 bp
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* 21663 21763: gap of 100 bp
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AC073035      AC073035      67729 bp      DNA      linear      HTG 08-JUN-2000
LOCUS      Homo sapiens chromosome 2 clone RP11-38301 map 2, LOW-PASS SEQUENCE
DEFINITION      SAMPLING.
ACCESSION      AC073035
VERSION      AC073035.1 GI-8347978
KEYWORDS      HTG; HTGS-PHASE0.
SOURCE      human.
ORGANISM      Homo sapiens
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 67729)
AUTHORS      Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE      Homo sapiens chromosome 2, clone RP11-38301
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 67729)
AUTHORS      Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
              Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bada, F.,
              Boguslavskiy, L., Boukhgalter, B., Brown, A., Burkett, G.,
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              Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J.,
              Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
              Young, G., Zainoun, J., Zimmer, A. and Zody, M.
DIRECT SUBMISSION
Submitted (08-JUN-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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Project Information
Center project name: LI0434
Center clone name: 383_O_1
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NOTE: This record contains 78 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
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* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
*
* 1      780: contig of 780 bp in length
* 81      880: gap of 100 bp
* 881      1643: contig of 763 bp in length
* 1644      1743: gap of 100 bp
* 1744      2514: contig of 771 bp in length
* 2515      2614: gap of 100 bp
* 2615      3382: contig of 768 bp in length
* 3383      3482: gap of 100 bp
* 3483      4258: contig of 776 bp in length
* 4259      4358: gap of 100 bp
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4359      5117: contig of 759 bp in length
5118      5217: gap of 100 bp
5218      6007: contig of 790 bp in length
6008      6107: gap of 100 bp
6108      6875: contig of 768 bp in length
6876      6975: gap of 100 bp
6976      7741: contig of 766 bp in length
7742      8623: gap of 100 bp
7842      8623: contig of 782 bp in length
8624      8723: gap of 100 bp
8724      9496: contig of 773 bp in length
9497      9596: gap of 100 bp
9597      10363: contig of 767 bp in length
10364      10463: gap of 100 bp
10464      11257: contig of 794 bp in length
11258      11357: gap of 100 bp
11358      12109: contig of 752 bp in length
12110      12209: gap of 100 bp
12210      12973: contig of 764 bp in length
12974      13073: gap of 100 bp
13074      13816: contig of 743 bp in length
13817      13916: gap of 100 bp
13917      14688: contig of 772 bp in length
14689      14788: gap of 100 bp
14789      15559: contig of 771 bp in length
15560      15659: gap of 100 bp
15660      16442: contig of 783 bp in length
16443      16542: gap of 100 bp
16543      17317: contig of 775 bp in length
17318      17417: gap of 100 bp
17418      18195: contig of 778 bp in length
18196      18295: gap of 100 bp
18296      19069: contig of 774 bp in length
19070      19169: gap of 100 bp
19170      19933: contig of 764 bp in length
19934      20033: gap of 100 bp
20034      20820: contig of 787 bp in length
20821      20920: gap of 100 bp
20921      21662: contig of 742 bp in length
21663      21762: gap of 100 bp
21763      22525: contig of 763 bp in length
22526      22625: gap of 100 bp
22626      23395: contig of 770 bp in length
23396      23495: gap of 100 bp
23496      24279: contig of 784 bp in length
24280      24379: gap of 100 bp
24380      25149: contig of 770 bp in length
25150      25249: gap of 100 bp
25250      26024: contig of 775 bp in length
26025      26124: gap of 100 bp
26125      26902: contig of 778 bp in length
26903      27002: gap of 100 bp
27003      27770: contig of 768 bp in length
27771      27870: gap of 100 bp
27871      28635: contig of 765 bp in length
28636      28735: gap of 100 bp
28736      29510: contig of 775 bp in length
29511      29610: gap of 100 bp
29611      30366: contig of 756 bp in length
30367      30466: gap of 100 bp
30467      31248: contig of 782 bp in length
31249      31348: gap of 100 bp
31349      32125: contig of 777 bp in length
32126      32225: gap of 100 bp
32226      32978: contig of 753 bp in length
32979      33078: gap of 100 bp
33079      33865: contig of 787 bp in length
33866      33965: gap of 100 bp
33966      34725: contig of 760 bp in length
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34826      35593: contig of 768 bp in length
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35694      36484: contig of 791 bp in length

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TITLE
 JOURNAL
 COMMENT


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Db 1715 GCCATAAATCTGTCAAGTCTGCTTTGACGGCTCATTTGCTAGAAATGGGCTTTG 1774
Qy 6035 atctcttttataattaagaactaaagtgtcttttttgtaagttaggttcagagaatcc 6094
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Qy 6095 attataaatgatctgaatgttccctaaa 6124
Db 1835 CATTATAAATGGTGTACAGAACTCCATGAA 1864

RESULT 6
LOCUS AX047362 3081 bp DNA linear PAT 15-DEC-2000
DEFINITION Sequence 48 from Patent WO0068380.
ACCESSION AX047362
VERSION AX047362.1 GI:11876608
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3081)
AUTHORS Bandman,O., Hillman,J.L., Tang,Y.T., Lal,P., Yue,H., Baughn,M.R.,
Lu,D.A. and Azimzal,Y.
TITLE Extracellular matrix and adhesion-associated proteins
JOURNAL Patent: WO 0068380-A 48 16-NOV-2000;
Incyte Genomics, Inc. (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 2850987CB1"
BASE COUNT 829 a 643 c 680 g 929 t
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Query Match 8.6%; Score 647.6; DB 6; Length 3081;
Best Local Similarity 91.5%; Pred. No. 2.9e-117;
Matches 686; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

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Qy 5435 ctctaaccatcagcttgaaatgagcaagagagcctactgtgctccagagtgctga 5494
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Qy 5975 gccataatctctgcagctgtctgtttgaggcgtcattgtctctagaatcggtaagaa 6034
Db 1690 GCCATAATCTCTGTCAAGTCTGCTTTGCGAGCGCTCATTTGCTGTAGAAATCGGCTTTG 1749
Qy 6035 atctcttttataattaagaactaaagtgtctttttgtaagttaggttcagagaatcc 6094
Db 1750 GTCCCTTTGTTAACTGTGCACACAGTGTCTGCAAGAAATGTAATGAATCTGAAAGAGG 1809
Qy 6095 attataaatgatctgaaatgttccctaaa 6124
Db 1810 CATTATAAATGGTGTACAGAACTCCATGAA 1839

RESULT 7
LOCUS AX086462 3333 bp DNA linear PAT 09-MAR-2001
DEFINITION Sequence 414 from Patent WO0112659.
ACCESSION AX086462
VERSION AX086462.1 GI:13275974
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3333)
AUTHORS Wiemann,S.
TITLE Human dna sequences
JOURNAL Patent: WO 0112659-A 414 22-FEB-2001;
German Human Genome Project (DE)
FEATURES
source Location/Qualifiers
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BASE COUNT 931 a 671 c 697 g 1034 t
ORIGIN
Query Match 8.6%; Score 647.6; DB 6; Length 3333;
Best Local Similarity 91.5%; Pred. No. 2.8e-117;
Matches 686; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

Qy 5375 ttcttaacagatactgagccaaacccctggagggaactcatctaatgggtgtgaaaga 5434
Db 1064 TTTACACAAAGATAGTACGCCAAACCCCTGGAGGGAACATCATCTAATGGGTGTGAAAGA 1123
Qy 5435 ctctaaccatcctcagcttgaaatgagcaagagagcctactgtgctccagatggctga 5494
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Qy 5495 gcccttcgctacctcccgatggatgggtctcctactacaaccagcctgtgttctggc 5554
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Qy 5615 gtagcctcacactcaggagactgagtggttccatcctcactagatttttgatgggagcagc 5674
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Db 1664 GCCATATCTCTGCTAGTCTGCTGTGTTCAGGCGTCAATGCTGCTAGATCGGCTTTG 1723

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Db 1724 GTCCTTTGATTAACTGTGACACAGTTGCTGCAGANAATGTAATTGAATCTGAAGAGG 1783

QY 6095 attaaataatgatctgaaattgttcctctaaa 6124
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RESULT 8
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LOCUS HSM801908 3333 bp mRNA linear PRI 10-MAR-2001
DEFINITION Homo sapiens mRNA; cDNA DKFp586J0624 (from clone DKFp586J0624);
complete cds.
ACCESSION AL136944
VERSION AL136944.1 GI:12053382
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3333)
AUTHORS Wiemann,S., Well,B., Wellenreuther,R., Gassenhuber,J., Glassl,S.,
Ansorge,W., Boecker,M., Bloeker,H., Bauersachs,S., Blum,H.,
Lauber,J., Duesterhoeft,A., Beyer,A., Koehrer,K., Strack,N.,
Mewes,H.W., Ottenwaelder,B., Obermaier,B., Tampe,J., Heubner,D.,
Wambutt,R., Korn,B., Klein,M. and Poustka,A.
TITLE Toward a Catalog of Human Genes and Proteins: Sequencing and
Analysis of 500 Novel Complete Protein Coding Human cDNAs
JOURNAL Genome Res. 11 (3), 422-435 (2001)
PUBMED 11230166
REFERENCE 2 (bases 1 to 3333)
AUTHORS Duesterhoeft,A., Lauber,J., Mewes,H.W., Gassenhuber,J. and
Wiemann,S.
TITLE Direct Submission
JOURNAL Submitted (18-JAN-2000) MIPS, Am Klopferspitz 18a, D-82152
Martinsried, GERMANY
COMMENT Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
LOCATION/Qualifiers
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BASE COUNT 931 a 671 c 697 g 1034 t
ORIGIN

Query Match 8.6%; Score 647.6; DB 9; Length 3333;
Best Local Similarity 91.5%; Pred. No. 2.8e-117;
Matches 686; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 5375 ttcttaacagatactagcacaacccctggaggactcatctaatcggctggaaga 5434
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QY 5495 gcccttcgctacctccagagatggatgggtctcctactacaacccagcctgtgtctcggc 5554
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Db 1184 GCCCTTCGGTACCTTCGGAGATGGATGGGTCTCCTACTACAACCAAGCGCTGTGTTCTGGC 1243

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QY 5615 gtacgcctacactcaggagactgagtggtccatcctcctcagttattttgagggagcaccgc 5674
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Db 1304 GTACGCCCTACACTCAGGAGCTGAGTGGTTCCATCCTCAGTATATTTGTATGGAGCATCAGC 1363

QY 5675 tataactggaataatagggaactgtagcttttacttgctcagtcacgtcgaataatggttctggt 5734
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Db 1364 TATAACTGGAAATAATGGAACTGTAGCTTTTACTTGGCTAGTCGAAATAATGTGTTGGT 1423

QY 5735 tcggacaggtctgatctcagagattggcacagcttctcgtttgatctctgtgtgatctc 5794
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QY 5855 aagttcattcaaggagagtcgaattacacctaccacgaataccctgaaattacaactgaaat 5914
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QY 5915 atacatgtctaaagggtcttaattctgtaattgttcccgagacagtgctgaactctgt 5974
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Qy 5975 gccataatctctgcaagtcgtctgttgcagggcgcattgctgctagaatacggttaagaa 6034
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Qy 6035 atctcttttatataataaactaaagtctcttttggtaagttaggttcagagaatcc 6094
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RESULT 9
AF231121 2443 bp mRNA linear PRI 20-MAR-2000
LOCUS Homo sapiens iron-regulated transporter IREG1 (IREG1) mRNA,
DEFINITION complete cds.
ACCESSION AF231121
VERSION AF231121.1 GI:7264728
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2443)
AUTHORS McKie,A.T., Marciani,P., Rolfs,A., Brennan,K., Wehr,K., Barrow,D.,
Miret,S., Bonford,A., Peters,T.J., Farzaneh,F., Hediger,M.A.,
Hentze,M.W. and Simpson,R.J.
TITLE A novel duodenal iron-regulated transporter, IREG1, implicated in
the basolateral transfer of iron to the circulation
Mol. Cell 5 (2), 299-309 (2000)
JOURNAL 20337919
MEDLINE
REFERENCE 2 (bases 1 to 2443)
AUTHORS McKie,A.T.
TITLE Direct Submission
Submitted (02-FEB-2000) Molecular Medicine, King's College London,
Guy's, King's and St. Thomas' Medical School, Rayne Institute 123
Coldharbour Lane, London SE5 9NU, UK
FEATURES
Location/Qualifiers
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up-regulated in hereditary haemochromatosis"
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BASE COUNT 618 a 533 c 559 g 729 t 4 others
ORIGIN

Query Match 8.6%; Score 646; DB 9; Length 2443;
Best Local Similarity 91.3%; Pred. No. 5.9e-117;
Matches 685; Conservative 0; Mismatches 65; Indels 0; Gaps 0;

Qy 5375 ttcttaacagatactgagccaaacccctggagggaactcatctaattgggtgtgaagaa 5434
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RESULT 10
AF215636 3317 bp mRNA linear PRI 02-JUL-2000
LOCUS Homo sapiens SLC11A3 iron transporter mRNA, complete cds.
DEFINITION
ACCESSION AF215636
VERSION AF215636.1 GI:8895484
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3317)
AUTHORS Abboud,S. and Haile,D.J.
TITLE A novel mammalian iron-regulated protein involved in intracellular
iron metabolism
J. Biol. Chem. 275 (26), 19906-19912 (2000)

[illegible]

Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L10999
Center clone name: 2054_E_23

* NOTE: This record contains 75 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

* 1
* 731 830: contig of 730 bp in length
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* 831 1580: contig of 750 bp in length
* 1581 1680: gap of 100 bp
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* 2397 2496: gap of 100 bp in length
* 2497 3260: contig of 764 bp in length
* 3261 3360: gap of 100 bp
* 3361 4111: contig of 751 bp in length
* 4112 4211: gap of 100 bp
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* 4917 5016: gap of 100 bp
* 5017 5753: contig of 737 bp in length
* 5754 5853: gap of 100 bp
* 5854 6607: contig of 754 bp in length
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* 6708 7387: contig of 680 bp in length
* 7388 7487: gap of 100 bp
* 7488 8249: contig of 762 bp in length
* 8250 8349: gap of 100 bp
* 8350 9064: contig of 715 bp in length
* 9065 9164: gap of 100 bp
* 9165 9900: contig of 736 bp in length
* 9901 10000: gap of 100 bp
* 10001 10744: contig of 744 bp in length
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* 12439 12538: gap of 100 bp
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Matches 660; Conservative 0; Mismatches 101; Indels 2; Gaps 2;

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Db 39514 GAACCTCAGCAGTAATAACAATGTTTAAAGTTTCCTTACACTTTAAACCATAAACCAT 39573

QY 6620 tattagtcattgaaacttaaaaataactagttacttatactataataggatttattatg 6679
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QY 6680 tctctgatttcaaaagttttgtttgttagtgaataatcacagaaaaacagaaactaaga 6739
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QY 6740 agttttagattagactcttcttctgtcgtgactgataaatacttatttagggccact 6799
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QY 6800 aataaccgaattatttattgaaataattcttaaggcaaggctatgtattttaag 6859
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QY 6920 gtgattgaaatgatcctgtgtaaaactaaaaatctaactttaaaaaaatattttattata 6979
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RESULT 12
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LOCUS AK002038 2286 bp mRNA linear PRI 31-AUG-2001
DEFINITION Homo sapiens cDNA FLJ11176 fis, clone PLACE1007386.
ACCESSION AK002038
VERSION AK002038.1 GI:7023677
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              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1 (bases 1 to 2286)
AUTHORS      Isogai,T., Ota,T., Hayashi,K., Sugiyama,T., Otsuki,T., Suzuki,Y.,
              Nishikawa,T., Nagai,K., Sato,H., Sugano,S., Shiratori,A., Sudo,H.,
              Wagatsuma,M., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H.,
              Sugawara,M., Takahashi,M., Chiba,Y., Ishida,S., Murakawa,K.,
              Ono,Y., Takiguchi,S., Watanabe,S., Kimura,K., Murakami,K.,
              Ishii,S., Kawai,Y., Saito,K., Yamamoto,J., Wakamatsu,A.,
              Nakamura,Y., Nagahara,K., Masuho,Y., Niinomiya,K. and Iwayanagi,T.
TITLE         NEDO human cDNA sequencing project
JOURNAL       Unpublished
REFERENCE     2 (bases 1 to 2286)
AUTHORS      Isogai,T. and Otsuki,T.
JOURNAL       Direct Submission
              Submitted (16-FEB-2000) Takao Isogai, Helix Research Institute,
              Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
              (E-mail:genomics@hri.co.jp, Tel:81-438-52-3951, Fax:81-438-52-3952)
COMMENT      NEDO human cDNA sequencing project supported by Ministry of
              International Trade and Industry of Japan; cDNA full insert
              sequencing: Research Association for Biotechnology; cDNA library
              construction, 5'- & 3'-end one pass sequencing and clone selection:
              Helix Research Institute (supported by Japan Key Technology Center
              etc.) and Department of Virology, Institute of Medical Science,
              University of Tokyo.
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Best Local Similarity 91.2%; Pred. No. 1.6e-114;
Matches 684; Conservative 0; Mismatches 64; Indels 2; Gaps 1;

QY 5375 ttcttaacagatactgagccaaacccctggagggaactcatctaatgggtgtaaga 5434
Db 36 TTTCACAAAGATACTAGCCAAAACCCCTGAGGGAACCTCATCTAATGGGTGTGAAGA 95

QY 5435 ctctaacatccatgagcttgaaatgaaagagcagcactacttctgctccccagatgctga 5494
Db 96 CTCTAACATCCATGAGCTTGAACATGAGCAAGAGCAGCTACTTGTGCTCCAGATGGCTGA 155

QY 5495 gccctccgtacctccagatgagtgatgggtctctactactaacaccagctgttcttcgc 5554
Db 156 GCCCTCCGTACCTCCGAGATGGATGGGTCTCTCTACTACCAACGAGCTGTGTTCTGGC 215

QY 5555 tggcatgggtcttcttccctttatgactgtcctggtgctgactgacatccaccag 5614
Db 216 TGGCATGGGCTTCTCTTCTTATATGACTGTCTCTGGGCTTTCACTCACACACAGG 275
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QY 5615 gtacgcctacactcagggaactgaagtggtccatctcctcagttatttggatgggagcatcagc 5674
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QY 5675 tataactgaaataatgggaactgtagcttttacttggtcagtcagtcgaaatgtggtttggt 5734
Db 336 TATAACTGGAATAATGGGAACGTGTAGCTTTTACTTTGGCTAGCTCGAATAATGGTGGTGGT 395
QY 5735 tcggacaggtctgatctcaggtatggcagacttccctgttggatcttctgtgtgatctc 5794
Db 396 TCGGACAGGTCGTGATCTCAGGATTTGGCAGAGCTTTCCGTGTTGATCTTGTGTGATCTC 455
QY 5795 tctattatcgcctggaagcccccctggaactgtccctttctctcttcttgaagatatccgatc 5854
Db 456 TGTATTTCATGCTCGTGAAGCCCTCGTGGTGTGCGTCTCTCTCTCTCTCTCTCTCTCTCT 515
QY 5855 aaggttcacagagagagatcaattacacctaccagataacctgaactgaactgaat 5914
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Db 754 CATTATAATGTGTACACAACTCCATGAA 783

RESULT 13
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LOCUS Homo sapiens full length insert cDNA clone YB21H04.
DEFINITION AF147322
ACCESSION AF147322
VERSION AF147322.1 GI:4761673
KEYWORDS FLI_CDNA.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
Woessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J.,
Marth,G., Bowles,L., Wylie,T., Bowers,Y., Steptoe,M., Theising,B.,
Geisler,S., Allen,M., Underwood,K., Chappell,J., Person,B.,
Gibbons,M., Harvey,N., Pape,D., Chamberlain,A., Morales,R.,
Schurk,R., Ritter,E., Kohn,S., Swaller,T., Behmer,K., Hillier,L.,
Wilson,R. and Waterston,R.
Full Clone Sequencing of the Longest Available Member from Each
UniGene Cluster
Unpublished
Waterston,R.
2 (bases 1 to 513)
Direct Submission
Submitted (30-APR-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
SUBMITTED BY:
Genome Sequencing Center
Department of Genetics
Washington University
St. Louis MO 63108, USA
http://genome.wustl.edu/gsc
mailto:est@watson.wustl.edu

NOTICE: This sequence represents the full insert of this cDNA. No
attempt has been made to verify whether this corresponds to the
```

full-length of the original mRNA from which it was derived. We have tried to obtain double-stranded, or double chemistry sequence across the entire clone, but potentially, there are areas in the sequence where this level of coverage was not achieved. Nevertheless, we are confident of the accuracy of this sequence as all regions of low quality, as defined by PHRAP (P. Green, in preparation), were visually inspected and edited accordingly. The consensus quality values for this sequence have been submitted separately.

similar to Arabidopsis thaliana protein AAC28758 (PID:g3395426) (AC004683) unknown protein

The location of this clone is unknown.

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Db 1 GGTCTTTGGCTCTTGTATTAACTGTGACACAGTGTGTCAGAAAGAAATGTAATTGAATCT 60
QY 7040 gaaagagcattataaagggtgtacagaactccatgaactatctctgattcttgcatt 7099
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QY 7100 ttcatcattgctcctcgtcccaaatcctgaagcttttggcttgcgtattgatttca 7159
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Db 181 GTCTCTTTTGGCAATGGGCCACATTTATGTTATTTCCGATTTGCCAAATAACTCTGGGA 240
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RESULT 14

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LOCUS Rattus norvegicus clone CH230-145018, *** SEQUENCING IN PROGRESS
DEFINITION *** 59 unordered pieces.
AC096437
VERSION AC096437.3 GI:17947216
KEYWORDS HTG; HTGS_PHASE1.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 (bases 1 to 172437)
Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
Alisbrooks,S.L., Amaratinge,H.C., Are,J.R., Banks,T., Barbaria,J.,
Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J.,
Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C.,
Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F.,
Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R.,
Chen,Z., Chowdry,I., Christopoulos,C., Cleveland,C.D., Cox,C.,
Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C.,
Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O.,
Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H.,
Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C.,
Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J.,
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Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzger,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Morgan,M., Morris,S., Moser,M., Neal,D., Newton,J., Newton,N.,
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Stinson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H.,
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Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R.,
Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C.,
Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S.,
Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Nelson,D.,
Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 172437)
Worley,K.C.

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Dec 20, 2001 this sequence version replaced gi:17062250.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GF00
Center clone name: CH230-145018
----- Summary Statistics
Assembly program: Phrap; version 0.990329First call to
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Consensus quality: 144276 bases at least Q40

Consensus quality: 151836 bases at least Q30
Consensus quality: 158483 bases at least Q20
Estimated insert size: 150873; sum-of-contigs estimation
Quality coverage: 0x in Q20 bases; agarose-fp estimation
Quality coverage: 2.2x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 59 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 13693: contig of 13693 bp in length
* 13793: gap of unknown length
* 13794: contig of 7716 bp in length
* 21510: gap of unknown length
* 21510: contig of 8893 bp in length
* 30502: gap of unknown length
* 30503: contig of 6736 bp in length
* 30603: gap of unknown length
* 37338: contig of 5704 bp in length
* 37339: gap of unknown length
* 43142: contig of 5704 bp in length
* 43143: gap of unknown length
* 43242: contig of 4598 bp in length
* 47841: gap of unknown length
* 47941: contig of 3858 bp in length
* 51798: gap of unknown length
* 51799: contig of 5864 bp in length
* 51899: gap of unknown length
* 57862: contig of 6875 bp in length
* 57863: gap of unknown length
* 64737: contig of 3813 bp in length
* 64838: gap of unknown length
* 68650: contig of 3263 bp in length
* 68651: gap of unknown length
* 68751: contig of 3263 bp in length
* 72013: gap of unknown length
* 72114: contig of 3954 bp in length
* 76068: gap of unknown length
* 76167: contig of 2748 bp in length
* 78915: gap of unknown length
* 78916: contig of 3747 bp in length
* 82762: gap of unknown length
* 82763: contig of 2235 bp in length
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* 85097: contig of 1973 bp in length
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* 107313: gap of unknown length
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* 113150: contig of 1131 bp in length
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LOCUS
DEFINITION Rattus norvegicus ferroportin 1 mRNA, complete cds.
ACCESSION AF394785
VERSION AF394785.1 GI:15021656
KEYWORDS
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 1949)
AUTHORS Yeh,K.-Y., Yeh,M. and Glass,J.
TITLE Iron induces ferroportin 1 (FPRI), clustering and redistribution in
rat intestinal epithelial cells
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1949)
AUTHORS Yeh,K.-Y., Yeh,M. and Glass,J.
TITLE Direct Submission
JOURNAL Submitted (23-JUN-2001) Department of Medicine and Feist-Weiller
Cancer Center, Louisiana State University Health Sciences Center,
1501 Kings Highway, Shreveport, LA 71130, USA
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Best Local Similarity	78.5%	Pred. No. 1.5e-83		
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Gaps				1

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Db 1590 ATCTCCGTCAAGCTGCTGTTTGCAGGAGTCACTGCTGCTAGAAATCGGCTCTTTGGTCTCTT 1649
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Search completed: July 23, 2002, 23:47:00
Job time: 25385 sec

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1	647.6	8.6	8.6	1861	20	AA30442	Human secreted protein
2	647.6	8.6	8.6	1861	22	AA59271	Human cDNA encoding
3	647.6	8.6	8.6	1861	24	AB40940	Human polynucleotide
4	647.6	8.6	8.6	2824	24	AA72731	Human cervical cancer
5	647.6	8.6	8.6	3081	22	AA66912	Human EXMAD-23 coding
6	647.6	8.6	8.6	3328	22	AA160076	Human polynucleotide
7	647.6	8.6	8.6	3454	22	AA138290	Human polynucleotide
8	647.4	8.6	8.6	3420	23	AA84449	DNA encoding novel
9	636	8.5	8.5	741	22	AA23122	Human breast cancer

```

PR 20-JAN-1999;      98US-0235609.
XX 22-JAN-1998;      98US-0072134.
XX                                     (GEMY ) GENETICS INST INC.
PA
XX
XX Agostino MJ, Clark HF, Collins-Racie LA, Fechtel K;
PI Jacobs K, Iavallie ER, McCoy JW, Merberg D, Steininger RJ;
PI Treacy M, Wong GG;
XX WPI; 1999-458682/38.
XX P-PSDB; AAY29327.
XX
XX New polynucleotides encoding secreted human proteins derived from,
PT e.g. fetal brain potentially used as immunostimulators
XX
XX Claim 15; Page 114-115; 139pp; English.
XX
CC The present sequence encodes a human secreted protein. Human secreted
CC protein polynucleotides and proteins are predicted to have biological
CC activities which would make them suitable for treating, preventing or
CC ameliorating medical conditions in humans and animals, although no
CC supporting data is given. Suggested activities include nutritional
CC activity, cytokine and cell proliferation/differentiation activity,
CC immune stimulating (e.g. as vaccines) or suppressing activity,
CC hematopoietic regulating activity, tissue growth activity,
CC activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, cadherin/tumour invasion suppressor activity, and tumour
CC inhibition activity. The polynucleotides are also stated to be useful
CC for gene therapy.
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Best Local Similarity 91.5%; Pred. No. 1.1e-108;
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XX	27-MAR-2001 (first entry)		
DT			
XX	Human EXMAD-23 coding sequence SEQ ID NO: 48.		

PR 11-MAY-1999; 99US-0133643.
PR 23-AUG-1999; 99US-0150409.
XX (INCY-) INCYTE GENOMICS INC.
XX Bandman O, Hillman JL, Tang YT, Lal P, Yue H, Baughn MR, Lu DAM;
PI Azimzai Y;
XX WPI: 2001-007395/01.
DR P-PSDB; AAB27245.
XX Isolated polynucleotide encoding extracellular matrix or
PT adhesion-associated protein (EXMAD) useful for diagnosing, treating, or
PT preventing disorders associated with expression of EXMAD such as
PT proliferative, immune and genetic disorders -
XX Claim 4; Page 127-128; 129pp; English.
XX The present invention provides the protein and coding sequences for 25
CC novel extracellular matrix and adhesion-associated proteins (EXMADS).
CC These are designated EXMAD-1, EXMAD-2, EXMAD-3, EXMAD-4, EXMAD-5,
CC EXMAD-6, EXMAD-7, EXMAD-8, EXMAD-9, EXMAD-10, EXMAD-11, EXMAD-12,
CC EXMAD-13, EXMAD-14, EXMAD-15, EXMAD-16, EXMAD-17, EXMAD-18, EXMAD-19,
CC EXMAD-20, EXMAD-21, EXMAD-22, EXMAD-23, EXMAD-24 and EXMAD-25. They are
CC useful in the prevention and treatment of cancers, cell proliferation, and
CC cardiovascular, reproductive, immune, musculoskeletal, developmental and
CC gastrointestinal disorders and inflammation.
XX Sequence 3081 BP: 829 A; 643 C; 680 G; 929 T; 0 other;
SQ

XX	Extracellular matrix and adhesion-associated protein; EXMAD; cancer;
KW	inflammation; reproductive disorder; cardiovascular disorder;
KW	immune disorder; musculoskeletal disorder; developmental disorder;
KW	gastrointestinal disorder; cell proliferation disorder; ss.
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XX	Homo sapiens.
OS	
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PN	WO2000068380-A2.
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PD	16-NOV-2000.
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XX	10-MAY-2000; 2000WO-US12811.
PF	
XX	


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RESULT 11
AAV59651
ID AAV59651 standard; DNA; 1540 BP.
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AC AAV59651;
XX
DF 19-JAN-1999 (first entry)
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DE Human secreted protein gene 141 clone HCM30.
XX
KW Human; secreted protein; fusion protein; gene therapy; protein therapy;
KW diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;
KW developmental abnormality; fetal deficiency; blood; allergy; renal; ds;
KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;
KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;
KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;
KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;
KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
XX
OS Homo sapiens.
XX
PN WO9839448-A2.
XX
PD 11-SEP-1998.
XX
PF 06-MAR-1998; 98WO-US04493.
XX
PR 02-OCT-1997; 97US-0061060.
PR 07-MAR-1997; 97US-0038621.
PR 07-MAR-1997; 97US-0040161.
PR 07-MAR-1997; 97US-0040162.
PR 07-MAR-1997; 97US-0040163.
PR 07-MAR-1997; 97US-0040333.
PR 07-MAR-1997; 97US-0040334.
PR 07-MAR-1997; 97US-0040336.
PR 07-MAR-1997; 97US-0040626.
PR 11-APR-1997; 97US-0043311.
PR 11-APR-1997; 97US-0043312.
PR 11-APR-1997; 97US-0043313.
PR 11-APR-1997; 97US-0043314.
PR 11-APR-1997; 97US-0043568.
PR 11-APR-1997; 97US-0043569.
PR 11-APR-1997; 97US-0043576.
PR 11-APR-1997; 97US-0043578.
PR 11-APR-1997; 97US-0043580.
PR 11-APR-1997; 97US-0043669.
PR 11-APR-1997; 97US-0043670.
PR 11-APR-1997; 97US-0043671.
PR 11-APR-1997; 97US-0043672.
PR 11-APR-1997; 97US-0043674.
PR 23-MAY-1997; 97US-0047492.
PR 23-MAY-1997; 97US-0047500.
PR 23-MAY-1997; 97US-0047501.
PR 23-MAY-1997; 97US-0047502.
PR 23-MAY-1997; 97US-0047503.
PR 23-MAY-1997; 97US-0047581.
PR 23-MAY-1997; 97US-0047582.
PR 23-MAY-1997; 97US-0047583.
PR 23-MAY-1997; 97US-0047584.
PR 23-MAY-1997; 97US-0047585.
PR 23-MAY-1997; 97US-0047586.
PR 23-MAY-1997; 97US-0047587.
PR 23-MAY-1997; 97US-0047588.
PR 23-MAY-1997; 97US-0047589.
PR 23-MAY-1997; 97US-0047590.
PR 23-MAY-1997; 97US-0047592.
PR 23-MAY-1997; 97US-0047593.
PR 23-MAY-1997; 97US-0047594.
PR 23-MAY-1997; 97US-0047595.
PR 23-MAY-1997; 97US-0047596.
PR 23-MAY-1997; 97US-0047597.
PR 23-MAY-1997; 97US-0047598.
PR 23-MAY-1997; 97US-0047599.
PR 23-MAY-1997; 97US-0047600.
PR 23-MAY-1997; 97US-0047601.
PR 23-MAY-1997; 97US-0047612.
PR 23-MAY-1997; 97US-0047613.
PR 23-MAY-1997; 97US-0047614.
PR 23-MAY-1997; 97US-0047615.
PR 23-MAY-1997; 97US-0047617.
PR 23-MAY-1997; 97US-0047618.
PR 23-MAY-1997; 97US-0047632.
PR 23-MAY-1997; 97US-0047633.
PR 06-JUN-1997; 97US-0048964.
PR 06-JUN-1997; 97US-0048974.
PR 13-JUN-1997; 97US-0049610.
PR 08-JUL-1997; 97US-0051926.
PR 16-JUL-1997; 97US-0052874.
PR 18-AUG-1997; 97US-0055724.
PR 22-AUG-1997; 97US-0056630.
PR 22-AUG-1997; 97US-0056631.
PR 22-AUG-1997; 97US-0056632.
PR 22-AUG-1997; 97US-0056636.
PR 22-AUG-1997; 97US-0056637.
PR 22-AUG-1997; 97US-0056662.
PR 22-AUG-1997; 97US-0056664.
PR 22-AUG-1997; 97US-0056845.
PR 22-AUG-1997; 97US-0056862.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056872.
PR 22-AUG-1997; 97US-0056874.
PR 22-AUG-1997; 97US-0056875.
PR 22-AUG-1997; 97US-0056876.
PR 22-AUG-1997; 97US-0056877.
PR 22-AUG-1997; 97US-0056878.
PR 22-AUG-1997; 97US-0056879.
PR 22-AUG-1997; 97US-0056880.
PR 22-AUG-1997; 97US-0056881.
PR 22-AUG-1997; 97US-0056882.
PR 22-AUG-1997; 97US-0056884.
PR 22-AUG-1997; 97US-0056886.
PR 22-AUG-1997; 97US-0056887.
PR 22-AUG-1997; 97US-0056888.
PR 22-AUG-1997; 97US-0056889.
PR 22-AUG-1997; 97US-0056892.
PR 22-AUG-1997; 97US-0056893.
PR 22-AUG-1997; 97US-0056894.
PR 22-AUG-1997; 97US-0056903.
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PR 22-AUG-1997; 97US-0056908.
PR 22-AUG-1997; 97US-0056909.
PR 22-AUG-1997; 97US-0056910.
PR 22-AUG-1997; 97US-0056911.
PR 05-SEP-1997; 97US-0057650.
PR 05-SEP-1997; 97US-0057659.
PR 05-SEP-1997; 97US-0057669.
PR 12-SEP-1997; 97US-0057761.
PR 12-SEP-1997; 97US-0058785.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;
PI Peng P, Ferrie AM, Fischer CL, Florence KA, Greene JM, Hu JS;
PI Kyaw H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;
PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;
XX
XX WPI; 1998-506364/43.
DR P-PSDB; AAW74869.
DR
XX
XX New isolated human genes and the secreted polypeptide(s) they encode
PT - useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders
XX
XX Claim 1; Page 375-376; 721pp; English.
XX
XX This sequence represents a nucleic acid molecule designated Gene 141
CC from the human cDNA clone HCM5H30 (deposited as clone ATCC 97902 and
CC ATCC 209048) which encodes a secreted human protein. The gene can be
CC used to generate fusion proteins by linking to the gene to a human
CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of
CC the fused protein as compared to the human protein only.
CC The invention relates to 186 novel genes and their fragments (nucleic
CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)
CC which are useful for preventing, treating or ameliorating medical
CC conditions e.g. by protein or gene therapy. Also, pathological
CC conditions can be diagnosed by determining the amount of the new
CC polypeptides in a sample or by determining the presence of mutations in
CC the new polynucleotides. Specific uses are described for each of the 186
CC polynucleotides, based on which tissues they are most highly expressed in
CC (see AAV59511 for described uses).
XX
XX Sequence 1540 BP; 404 A; 325 C; 343 G; 466 T; 2 other;
SQ

Query Match 8.3%; Score 624.6; DB 19; Length 1540;
Best Local Similarity 91.2%; Pred. NO. 1.6e-104;
Matches 685; Conservative 0; Mismatches 64; Indels 2; Gaps 2;
QY 5375 ttcttaacagatagctgagccaaacccctggagggaactcatctaatagggtgtaaga 5434
Db 230 ttacacaaagatgactgagccaaacccctggagggaactcatctaatagggtgtaaga 289
QY 5435 ctctaactcatgagcttgaaacatgagcaagcctcactgtgctccacagatggctga 5494
Db 290 ctctaactcatgagcttgaaacatgagcaagcctcactgtgctccacagatggctga 349
QY 5495 gcccttcgtaccttcgagatggatgggtctctactactacacacagcctgtgttctggc 5554
Db 350 gcccttcgtaccttcgagatggatgggtctctactactacacacagcctgtgttctggc 409
QY 5555 tggcatgggtctgtcttctctatagctgctcctgggtttgactgcatcacacagg 5614
Db 410 tggcatgggtctgtcttctctatagctgctcctgggtttgactgcatcacacagg 469
QY 5615 gtaagcctacactcaggagctaggt-ggttcactcctcagatatttgaatggagcatcag 5673
Db 470 gtaagcctacactcaggagctaggt-ggttcactcctcagatatttgaatggagcatcag 529
QY 5674 ctataactggaataaagggaactgtagcttttacttggtcagctcgaaatggtgttgg 5733
Db 530 ctataactggaataaagggaactgtagcttttacttggtcagctcgaaatggtgttgg 589
QY 5734 ttcggacaggctgctgactcaggaattggacacagcttctctgttctgtgtgatct 5793

Db 590 ttcggg-cagggtctgactcaggtattggcacagctttctctgttggatcttgtgtgatct 648
QY 5794 ctgtattcatgcttggaagcccccctggactgttcgtcttctccttttgaagataccgat 5853
Db 649 ctgtattcatgcttggaagcccccctggactgttcgtcttctccttttgaagataccgat 708
QY 5854 caaggttcattcaaggagagtgacttaattacacactacacagatcacctgaaattacaactgaaa 5913
Db 709 caaggttcattcaaggagagtgacttaattacacactacacagatcacctgaaattacaactgaaa 768
QY 5914 tatacatgtctaattgggtcttaattctgctaatttgcctggagacaaagtcctgaaatctg 5973
Db 769 tatacatgtctaattgggtcttaattctgctaatttgcctggagacaaagtcctgaaatctg 828
QY 5974 tgccataaactctctgcagctcgtgtttgcaggcgtcattgctgcagaaatcggtgaaga 6033
Db 829 tgccataaactctctgcagctcgtgtttgcaggcgtcattgctgcagaaatcggtgtttt 888
QY 6034 aatctcttttatataatgaactaaagtgtctttttgtaatgtaggttcagagaatc 6093
Db 889 ggtccttggatttaactgtgacacagctgtgctgcaagaaaatgtaattgaaatctgaaagag 948
QY 6094 cattataaataatgactgaaatgttccctaaa 6124
Db 949 gcattataaattggtgtacagaactcccatgaa 979
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AAH07857
ID AAH07857 standard; cDNA; 683 BP.
XX
XX AAH07857;
AC
XX 26-JUN-2001 (first entry)
DT
XX Human cDNA clone (5'-primer) SEQ ID NO:4692.
DE
XX Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
KW
XX Homo sapiens.
OS
XX EP1074617-A2.
PN
XX 07-FEB-2001.
PD
XX 28-JUL-2000; 2000EP-0116126.
PF
XX 29-JUL-1999; 99JP-0248036.
PR 27-AUG-1999; 99JP-0300253.
PR 11-JAN-2000; 2000JP-0118776.
PR 02-MAY-2000; 2000JP-0183767.
PR 09-JUN-2000; 2000JP-0241899.
XX
XX (HELI-) HELIX RES INST.
PA
XX
XX Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
XX WPI; 2001-318749/34.
XX
XX Primer sets for synthesizing polynucleotides, particularly the 5602
PT full-length cDNAs defined in the specification, and for the detection
PT and/or diagnosis of the abnormality of the proteins encoded by the
PT full-length cDNAs -
XX
XX Claim 1; SEQ ID 4692; 2537pp + CD ROM; English.
PS
XX The present invention describes primer sets for synthesizing 5602
CC full-length cDNAs defined in the specification. Where a primer set
CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC to the complementary strand of a polynucleotide which comprises one of
CC the 5602 nucleotide sequences defined in the specification, where the

CC polypeptides are also useful for isolating compounds with cytostatic
CC activity.

xx
SQ Sequence 657 BP; 165 A; 175 C; 122 G; 192 T; 3 other;

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Query Match          7.2%; Score 537.2; DB 22; Length 657;
Best Local Similarity 91.2%; Pred. No. 1.1e-88;
Matches 629; Conservative 0; Mismatches 20; Indels 41; Gaps 4;

Qy 113 ggaagaaagaaatccctcgggcccc-----tttctttttttctttccaaagtcgctcg 166
    |||||
Db 657 GGAAGAAAGAAATCCCTCGGGCCCNCTTTTCTTTGTTCTTTCCTCCAAAAGTCGTCG 598

Qy 167 ttgtagtc-ttttgcocaaaggtgtgtgttttttagaggtgtatctccagttccctgc 225
    |||||
Db 597 TTGTAGTCTTTTGTGCCCAAGNCGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 538

Qy 226 act-cctgttaacagcactcagcagcagcagcagcagcagcagcagcagcagcagcagc 284
    |||||
Db 537 ACTCCCTGTAAACAGCACCTCAGCGAGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 478

Qy 285 cagcgggtgcctcctagtcctcagcggcgaggagatcacacaccccgagagaggtgct 344
    |||||
Db 477 CAGCGGGTCCCTAGTGTCTATGACCGGGCGGAGATCACACCCCGCAGAGAGGTGCT 418

Qy 345 gtgtgagtgctcgtgacccgaaacatatgtgtgaaaccccggtgggcttttgagacaa 404
    |||||
Db 417 GTGGTGTAGTGTCTGTACCGAAGCATATGTGGAAACCCAGGTGGGGCTTTGGAGACAA 358

Qy 405 gcaactctaccggagttctggaggaatgtggctctgtgtgaaccatagctttgtaaaaa 464
    |||||
Db 357 GCAACTCTACACAGAGTCTGTGAGGAATGTGGCTCTGTGTGAACCATAGCTTTGTAAAA 298

Qy 465 gatcctttgactcatattgttgacgttaaggaagaaagaaatcaggggtgaggaaa 524
    |||||
Db 297 GATCCTTTGACTCATATTTGTGGACGTTAGGAAAGAAAGAAATTCAGGGTGTGGGAAA 238

Qy 525 aggggtttgcacagcgacggtgagtagattggcgagtttggtgattgccttgtaaa 584
    |||||
Db 237 AGGGGTTTGCACACAGGCTCGGATGGAGTAGATTGGGCAGTTTGGATTGCCCTTGTGTAAA 178

Qy 585 aaagaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaaacaa 644
    |||||
Db 177 AAAGAAACAAAA-----CAAAACAAACCAACCA 151

Qy 645 acccaaaagaaatgctgaacaaagagttctctctgtatgtgaaatgtgaagtgggc 704
    |||||
Db 150 ACCCAAAAAGAAATGCTGAACACAGAGTTTCTTACATGTATGTGAAATGTGAAGTTGGGC 91

Qy 705 agttattgactagtgtaataactgaattagtgtaattagtgtaattagtgtaataacatc 764
    |||||
Db 90 AGTTATTGACTAGGTCAATAACTGAATTTAGTGAATGGTATTAAAGTGAACGAAATACATC 31

Qy 765 ggttcattagtgtaactgataaaatgtaagt 794
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Db 30 GGTTCATAGGTAAGTGTATAAAATGTACCT 1
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Search completed: July 23, 2002, 23:48:05
Job time: 22025 sec

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PREMIUM 13

Query Match 3.4%; Score 257.4; DB 4; Length 14796;
Best Local Similarity 88.6%; Pred. NO. 2.9e-49;
Matches 279; Conservative 0; Mismatches 36; Indels 0; Gaps

Qy	4816	cgatcttggtcactgcaagctctgctctctctggttcaagccattctctctgcctcagcct	4875
Db	8873	CGATCTCGGCTCAGAGAAAGTCACCTCCAGGTTTCAGCGCATCTCTGCTCAGCCT	8814
Qy	4876	cccagtagctgggatgcaggcatccacacacaccccggttaatttttgattttta	4935
Db	8813	CCCAGATAGCTGGGACATACAGGCCGCCACACGCCAGCTAAATTTTGTATTTTTTA	8754
Qy	4936	gtagagacgggggttcaccatgttagccagatggtcttgatctcctgcactcgatct	4995
Db	8753	GTAAGACGGGGTTTACCATGTTAGCCAGATGGTCTCGATCTCTGACCTCGTGATCC	8694
Qy	4996	gccgcctcggctcccaagtgctggattacagggtgagccacgctgcctggccaat	5055
Db	8693	ACCGCCTCGGCCCTCCCAAGATGCTGGATTACAGGCGTGAGCCACCATGCCCGGCGCTG	8634
Qy	5056	acgctgtgtttttttt	5070
Db	8633	AAAGCTACTTTTCT	8619

SECRET

Query Match	3.4%	Score	257.4;	DB 4;	Length	14796;	
Best Local Similarity	88.6%;	Pred. No.	2.9e-49;				
Matches	279;	Conservative	0;	Mismatches	36;	Indels	0;
						Gaps	0;

[illegible]

QY	4936	4995
DB	GTAGAGCGGGTTTCAACCATGTTAGCAGGATGGTCTGATCTCCTGACCTCGTGATCT	8694
DB	GTAAAGACGGGGTTTCAACCATGTTAGCAGGATGGTCTGATCTCCTGACCTCGTGATCT	8694

Qy	4996	gcccgcctcgccctcccaagtctgggatactacaggtgtgagccacgctgctggccaat	5055
Db	8593	ACCCGCTCGGGCTCCCAAAGTCTGGGATACAGCGTGAGCCACCATGCCCGCCCTG	8634

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QY 5056 acgctgtgtttttt 5070
| | | | |
Db 8633 AAAGTCTACTTTTCT 8619

RESULT 14
US-09-496-694B-3/c
; Sequence 3, Application US/09496694B
; Patent No. 6335194
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Eric E. Swayze
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF SURVIVIN EXPRESSION
; FILE REFERENCE: ISPH-0439
; CURRENT APPLICATION NUMBER: US/09/496,694B
; CURRENT FILING DATE: 2000-02-02
; PRIOR APPLICATION NUMBER: 09/286,407
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 09/163,162
; PRIOR FILING DATE: 1998-09-29
; NUMBER OF SEQ ID NOS: 249
; SEQ ID NO 3
; LENGTH: 14796
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2811)...(2921)
; NAME/KEY: CDS
; LOCATION: (3174)...(3283)
; NAME/KEY: CDS
; LOCATION: (5158)...(5275)
; NAME/KEY: CDS
; LOCATION: (11955)...(12044)
; US-09-496-694B-3

Query Match 3.4%; Score 257.4; DB 4; Length 14796;
Best Local Similarity 88.6%; Pred. No. 2.9e-49;
Matches 279; Conservative 0; Mismatches 36; Indels 0; Gaps 0;

QY 4756 tgttttttttttttgagacagagtctcgtctgtgtgcccaggtggaagtgcagtgggcg 4815
| | | | |
Db 8933 TTTTGTGAGACGGAGTCTCGTCTGTGCGCCAGGCTGGAGTGCAGTGGCG 8874

QY 4816 cgaatcttggtcactcaagctctgctcctcctgggttcacgcacattctcctgctcagcct 4875
| | | | |
Db 8873 CGATCTCGGCTCACAGCAAGCTCCACCTCCAGGTTTCAGGCCATTCTCCTGCTCAGCCT 8814

QY 4876 cccaagtagctgggattgcaggcatccacacaccccgctaatgtttgtatttta 4935
| | | | |
Db 8813 CCGAGTAGCTGGACTACAGGCGCCGCCACACGCCAGCTAAATTTTGTATTTTTA 8754

QY 4936 gtagacaggggtttccaccatgttagccaggatggcttctgattcctcctgacctgtgatct 4995
| | | | |
Db 8753 GTAAACACGGGTTTCAACCATGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGATCC 8694

QY 4996 gccgcctcggcctcccaagtgctgggattacagagtgtagccaccgtgcttgccaat 5055
| | | | |
Db 8693 ACCCGCTCGGCTCCCAAAGTCTGGGATTACAGGCGTGAGCCACCATGCCCGGCCCTG 8634

QY 5056 acgctgtgtttttt 5070
| | | | |
Db 8633 AAAGTCTACTTTTCT 8619

RESULT 15
US-09-385-982-128
; Sequence 128, Application US/09385982
; Patent No. 6262334
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; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 128
; LENGTH: 588
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(588)
; OTHER INFORMATION: n = A,T,C or G
; US-09-385-982-128

Query Match 3.4%; Score 254.6; DB 4; Length 588;
Best Local Similarity 87.6%; Pred. No. 2.9e-49;
Matches 275; Conservative 0; Mismatches 39; Indels 0; Gaps 0;

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| | | | |
Db 21 ttttttttttttttgagcaggagtctcaactctgtcacccaggctggagtcagtggc 80

QY 4815 ggaatcttggtcactgcaagctctcctcctgggttcacgcacattctcctgctcagcc 4874
| | | | |
Db 81 atgactctggtcactgcaagctctcctcctgggttcacgcacattctcctgctcagcc 140

QY 4875 tcccaagtagctgggattgcaggcatccacacaccccgctaatgtttgtatttt 4934
| | | | |
Db 141 tctgtagtagctgggactacaggcgctccgccacacagccagctaatgtttgtatttt 200

QY 4935 agtagacaggggtttccaccatgttagccaggatggcttctgattcctcctgacctcgtgac 4994
| | | | |
Db 201 ggtanacaggggtttccaccngtttagccaggatggnctccatctcctgacctcgtgac 260

QY 4995 tgccgcctcggcctcccaagtgctgggattacagagtgtagccaccgtgctggccaa 5054
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Db 261 tgccacacctcggcctcccaagtgctgggattacagagtgtagccaccgtgctggccag 320

QY 5055 tacgctgtgttttt 5068
| | | | |
Db 321 gatggtatattttt 334

Search completed: July 24, 2002, 00:05:20
Job time: 26245 sec
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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: July 23, 2002, 16:43:00 ; Search time 7392.1 Seconds
(without alignments)
13686.662 Million cell updates/sec

Title: US-09-715-927-7
Perfect score: 7496
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Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 3: em_estin:*
- 4: em_estnu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_hic:*
- 12: gb_gss:*
- 13: em_gss_hum:*
- 14: em_gss_inv:*
- 15: em_gss_pln:*
- 16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	612.4	8.2	683	9 AU137852	AU137852 AU137852
3	603.8	8.1	875	10 BG536539	BG536539 602564946
C 4	598.6	8.0	913	9 AL543564	AL543564 AL543564
5	579.6	7.7	911	10 BF574374	BF574374 602131579
6	543.4	7.2	631	10 BG924298	BG924298 HNC26-1-D
7	519.2	6.9	810	9 AU133566	AU133566 AU133566
8	519.2	6.9	896	9 AU505078	AU505078 AU505078
9	505.6	6.7	771	9 AU134630	AU134630 AU134630
10	500.6	6.7	618	9 AW963336	AW963336 EST375409
11	496.2	6.6	732	10 BI835465	BI835465 603087579
C 12	494.4	6.6	859	9 AL577308	AL577308 AU577308
C 13	491.6	6.6	572	12 AQ728706	AQ728706 HS_5479_A
14	488	6.5	727	10 BG618204	BG618204 602645928
15	482.2	6.4	731	9 AV704855	AV704855 AV704855
16	470	6.3	513	10 BI002788	BI002788 PM0-HN007
17	455.6	6.1	938	9 AL545521	AL545521 AL545521

18	453	6.0	3071	11 AK008700	AK008700 Mus muscu
19	450.8	6.0	932	10 BG286556	BG286556 602382558
C 20	449.4	6.0	451	9 AA563938	AA563938 nk23b12.s
21	443.8	5.9	586	10 BG689712	BG689712 337909 BA
22	435.8	5.8	776	10 BI835692	BI835692 603087679
23	432.4	5.8	567	10 BG942981	BG942981 ax32b06.x
C 24	431.8	5.8	456	9 AI248642	AI248642 gh77d05.x
C 25	425.2	5.7	481	9 AW167802	AW167802 xg56e08.x
C 26	425	5.7	433	9 AI539532	AI539532 tp32a11.x
27	421.6	5.6	726	9 AU138245	AU138245 AU138245
C 28	419.8	5.6	448	9 AW450389	AW450389 UI-H-BT3-
29	418.6	5.6	665	9 BB623179	BB623179 BB623179
C 30	418	5.6	443	9 AI127313	AI127313 qb74g09.x
C 31	414.2	5.5	434	9 AI874113	AI874113 wmd4b10.x
32	410.6	5.5	565	10 W23461	W23461 zb33c01.r1
33	406.4	5.4	439	9 AL559331	AL559331 DKFZp313F
34	404	5.4	987	9 AL551987	AL551987 AL551987
35	403.4	5.4	431	9 AA226177	AA226177 nc26c06.s
36	390.4	5.2	1054	10 BF788989	BF788989 602104833
C 37	387.2	5.2	401	9 AI973210	AI973210 wr53b01.x
C 38	387	5.2	425	9 AA226521	AA226521 nc26c05.r
39	383.4	5.1	752	10 BI158667	BI158667 602921742
C 40	375	5.0	759	9 AL572951	AL572951 AL572951
41	363.4	4.8	434	10 D82422	D82422 HUMHBC4609
42	349	4.7	349	9 AA386154	AA386154 EST99917
43	348	4.6	515	10 D63209	D63209 HUM506F01B
44	347	4.6	563	9 AA490669	AA490669 zw99f10.r
45	341.2	4.6	603	10 BI460172	BI460172 603201763

ALIGNMENTS

RESULT 1
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LOCUS BE069938 624 bp mRNA linear EST 09-JUN-2000
DEFINITION RC4-BT0311-250200-014-b06 BT0311 Homo sapiens cDNA, mRNA sequence.
ACCESSION BE069938
VERSION BE069938.1 GI:8409134
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 624)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bata,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC4-BT0311-250
200-014-b06&st3=2000-02-25&st4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 623.
Location/Qualifiers
source 1..624
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/db_xref="taxon:9606"
/clone_lib="B70311"
/dev_stage="Adult"
SmaI; A mini-library was made by cloning libraries derived
from ORESTES PCR (U.S. Letters Patent application No. 196
716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      192 a      146 c      147 g      139 t
ORIGIN
Query Match      8.2%; Score 614.2; DB 9; Length 624;
Best Local Similarity 99.5%; Pred. No. 1.2e-74;
Matches 616; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 5415 catctaatgggtgtaagagactctaacatccatgagcttgagcttgaaacatgagacagagcctact 5474
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Db 624 CATCTAATGGGTGTGAAAGACTCTGACATCCATGAGCTGTGTACATGACGACGAGCCTACT 565
QY 5475 tgtgctccagatgctgagccctccgctaccctccgagatggatgggtccctactac 5534
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Db 564 TGTGGCTCCAGATGGCTGAGCCCTCCGTACTCTCCGAGATGGATGGGTCTCCTACTAC 505
QY 5535 aaccgacctgtttcttgctggctgagctggtctgtcttcccttatactgactgctcctggc 5594
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Db 504 AACCAGCCTGTGTTCTGGCTGGCATGGCTGTGCTTCTTTATATGATGATGCTGCTGGGC 445
QY 5595 tttagactcatcacacagggtaacccctacacacacagggactgagtggttccatccactcagt 5654
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Db 444 TTGTGACTGCATCACACAGGGTACGCCCTACACTCAGGACTGAGTGGTTCATCCTCAGT 385
QY 5655 atttgatggagcatcagctataactgaaataatggaactgtgacttttacttggcta 5714
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Db 384 ATTTTGATGGGAGCATACGATATAACTGGAATATGGGAACGTAGCTTTACTTTGGCTA 325
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Db 324 CGTCGAAAATGTGGTTGGTTCGGACAGTCTGATCTCAGGATGGCACAGCTTTCCCTGT 265
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Db 204 CTTTTGAGATATCCGATCAAGGTTCAATTCNAGGAGAGTCAATTTACACCTACCAAGATA 145
QY 5895 cctgaaatacaactgaaataacatgtctaatgggtctaatctctgtaattgtctcccg 5954
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Db 144 CCGTGAATTTACAACGTAAATATACATGTCTAATGGGTCTAATTCGTCTAATATTTGCCCG 85
QY 5955 gagacaagtctgaatctgtgccataatctctgacgtctgctgtttgcaaggcgtaatt 6014
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QY 6015 gctgctagaatcgggtaaga 6033
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Db 24 GCTGCTAGANTCGGTACAGA 6
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LOCUS AUI37852 683 bp mRNA linear EST 25-OCT-2000
DEFINITION AUI37852 PLACE1 Homo sapiens cDNA clone PLACE1007386 5', mRNA
sequence.
ACCESSION AUI37852
VERSION AUI37852.1 GI:10999373
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 683)
Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
Isogai,T.
HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix
Research Institute; cDNA library construction; Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
1. 683
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Best Local Similarity 98.3%; Pred. No. 2.1e-74;
Matches 628; Conservative 0; Mismatches 9; Indels 2; Gaps 1;
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Db 96 CTCATACATCATGAGCTTGAACATGAGCAGAGCCTACTTGTGGCTCCAGATGGCTGA 155
QY 5495 gcccttcgctaccctccagatgagtggtctcctactacaacacagcctgtgttctggc 5554
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Db 156 GCCCTTCGGTACCTCCAGATGGATGGGTCTCTCTACTACAACACAGCCTGTGTTCTGGC 215
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Db 216 TGGCATGGGTCTGTCTTCTCTTATATGACTGTCTCTGGCTTTGACTGCATCACACAGG 275
QY 5615 gtacgctacactcagggactgagtggtccatccctcagttatttgaaggagcagcagc 5674
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Db 276 GTACGCTTACACTCAGGACTGAGTGGTTCCTCATCTCTAGTATTTGATGGGACATCAGC 335
QY 5675 tataactggaataatgggaacttagcttttacttggctacgtogaaaaatgtggttgggt 5734
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Db 336 TATAACTGGAATAATGGAACTGTAGCTTTTACTTGGCTACGTTCGAAAAATGTGTTGGT 395
QY 5735 tcggacaggtctgatctcaggatggacacgttccctgtttgatctctgtgtgatctc 5794
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Db 396 TCGGACAGGTCTGATCTCAGGATTTGGCACAGCTTTCCTTGTGTGTGTGATCTC 455
QY 5795 tgtattcatgctggaagcccccctggacttgcgtttctctcttttgaagatcatccgac 5854
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Db 456 TGTATTTCATGCTGGAAGCCCCCTGGACTTGTCCGTCTCTCTTTGAAGATATCCGATC 515
QY 5855 aaggttcaatcaagagagtgtaattacacacctaccaagataacctgaaattacaactgaaat 5914
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Db 516 AAGGTCTATTCAAGGAGAGTCAATTACACCTACCAAGATACCTGAAATTTACAACGTAA-- 573
QY 5915 atacatgtctaatgggtctaatcttctgtaattatgtgtccggagacaaagtctcgtatcgt 5974
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Db	574	ATACATGCTCTAATGGGCTTAATTCCTGCTAATATTGTCCTCCGGAGACAAANTCCTGAATCTGT	633
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Db	634	CCCCATAATCTCTGTCANTCTGCTGTTTGGCANGCCTCAT	672
RESULT	3		
LOCUS	BG536539		
DEFINITION	602564946f1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4689562 5', mRNA sequence.	875 bp	linear EST 03-APR-2001
ACCESSION	BG536539		
VERSION	BG536539.1	GI:13528085	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 875)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-femail.nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI505 row: 1 column: 11 High quality sequence stop: 739.		
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source	1..875		
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	/clone="IMAGE:4689562"		
	/clone_lib="NIH_MGC_77"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggcgccctgcgc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CAGCGCCATATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGGCACATG-dt(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."		
BASE COUNT	204 a 193 c 205 g 273 t		
ORIGIN			
Query Match	8.1%;	Score 603.8;	DB 10; Length 875;
Best Local Similarity	98.1%;	Pred. No. 2.9e-73;	
Matches	61;	Conservative 0;	Mismatches 12; Indels 0; Gaps 0;
Qy	5425	gtgtgaagactctaacatccatgagcttgagatgagcagcctacttgcctccc	5484
Db	1	GTGTGAAGACTCTAACATCCATGAGCTTGAAATGAGCAGAGCTACTTGTGCTGCC	60
Qy	5485	agaaggctgagcccttcgtagctccgagatgatgggtctcctactacaacagcctg	5544
Db	61	AGATGGCTGAGCCCTTCGGTACCTCCGAGATGATGGGTCTCTACTACAAACAGCTG	120
Qy	5545	tgtttcggctggcatgggtcttcttcccttatatgactgctcgtggctttgactgca	5604
Db	121	TGTTTCTGGCTGGCATGGGCTCTGCTTTCCCTTTATATGACATGCTCTGGGCTTTGACTGCA	180
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Matches 616; Conservative 2; Mismatches 12; Indels 1; Gaps 1;

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QY 5477 tgcctcccagatgggtgagccctccgtacacctccgagatcgatgggtctctactacaa 5536
|:|||||||||
Db 853 TGCCCTCCAGATGGGTGAGCCCTCCGTACCTCCCGAGATGGAT-GGTCTCCTACTACAA 795
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QY 5537 ccagcctgtttctggctggcatgggtcttcttcttcttcttcttcttcttcttctt 5596
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Db 794 CCAGCGTGTGTTCTGGCTGGCATGGGTCTTCTCTTCTTATATACATGCTCCTGGGCTT 735
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QY 5597 tgactgcataccacagaggtgagctcactcagagactgagctggttccatctcagtat 5656
|:|||||||||
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QY 5657 ttgatgggagcatcagctataactgggaataatgggaactgtagcttttcttcttct 5716
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Db 674 TTTGATGGGAGCATCAGCTATAACTGGAATAATGGAACTGTAGCTTTTACTTGGCTAGC 615
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QY 5717 tcgaaaatgtgttgggtcggaaggtctgatctcagagattggcacaggttctctgttt 5776
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Db 614 TCGAAATGTGTTGGTTCGACAGGTCTGATCTCAGGATTTGGCACAGCTTTCTCTGTTT 555
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QY 5777 gatctgtgtgactctctgtattcatcgtggaagccccctggacttgcgtttcttccc 5836
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Db 554 GATCTGTGTGTGATCTCTGTATTCATGCTCGGAAGCCCCCTGGAGCTTGTCCGTTTCCTC 495
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QY 5897 tgaattacaactgaaataacatgtctaatgggtctaatcttcttcttcttcttcttcc 5956
|:|||||||||
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QY 5957 gacaagtcctgaactctgcccataatctctcagctcagctgttgcagcgctcatg 6016
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Db 374 GACAAGTCTGATCTGTGCCATTAATCTCTCAGTCTGCTGTTTGGCAGGCTCATGTC 315
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QY 6017 tgctgaatcggtaagaatctcttcttata 6047
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Db 314 TGCHAGAATCGGCTTTGGTCTCTTTGATTTA 284
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RESULT 5
BF574374
LOCUS 911 bp mRNA linear EST 12-DEC-2000
DEFINITION 602131579F1 NIH_MGC_81 Homo sapiens cDNA clone IMAGE:4271059 5',
mRNA sequence.
ACCESSION BF574374
VERSION BF574374.1 GI:11648086
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 911)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-re@mail.nih.gov
Tissue Procurement: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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High quality sequence stop: 632.
Location/Qualifiers
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/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: muscle (skeletal); Vector: pDNR-LIB
(Clontech); Site_1: SfiI (ggccctcggcc); Site_2: SfiI
(ggccattatggcc); 5' and 3' adaptors were used in cloning
as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCCC-3'
and 3' adaptor sequence:
5'-ATTCTAGAGCGGAGCGCGGCAGATG-dT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size
1.55 kb (range 1.0-4.0 kb). 15/15 colonies contained
inserts by PCR. This library was enriched for full-length
clones and was constructed by Clontech Laboratories (Palo
Alto, CA)."
BASE COUNT 214 a 222 c 228 g 247 t
ORIGIN

Query Match 7.7%; Score 579.6; DB 10; Length 911;
Best Local Similarity 97.2%; Pred. NO. 5.7e-70;
Matches 632; Conservative 0; Mismatches 14; Indels 4; Gaps 4;

QY 5375 ttcttaacagatactgagcaaaacccctggaggaactcaatcctaagggtgtgaaaga 5434
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|:|||||||||
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QY 5495 gccctccgtacctccagatggatgggtctcctactacaacaccagcctgttctctggc 5554
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Db 137 GCCCTTCGGTACTCTCCGAGATGGATGGTCTCTCTACTACAAACCAGCTGTGTTTCTGSC 196
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QY 5555 tggcatgggttctgttcttcttcttcttcttcttcttcttcttcttcttcttcttctt 5614
|:|||||||||
Db 197 TGGCATGGGTCTTGTCTTCTCTTATATGACTGTCTCTGGCTTTTGACTGCATCACCACAGG 256
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QY 5615 gtaecgctacactcagggactgagtggttccatcctcagttatttggatgggagcatcagc 5674
|:|||||||||
Db 257 GTACGCTTACACTCAGGACTGAGTGGTTCATCTCAGTATTTTGATGGGAGCATCAGC 316
|:|||||||||
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|:|||||||||
Db 436 TGTATTCAATGCTGGAAAGCCCCCTGGACTTGTCCGTTTCTCTCTTTTGAAGATATCCGATC 495
|:|||||||||
QY 5855 aaggttcttcaagagagtgatcaattacacctaccagataacctgaaattacaactgaaat 5914
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Db 496 AAGGTTTCAATCAAGGAGAGTCAATTTACACCTACCAAGATACCTGAAA-TACAACATGAAAT 554
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QY 5915 atacatgtcctaagggtcttaattctgtctaattatgtcccgagagacaagctcctgaatcgt 5974
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|:|||||||||
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RESULT 6
BG924298      631 bp      mRNA      linear      EST 06-NOV-2001
LOCUS      HNC26-1-D1.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
DEFINITION      sequence.
ACCESSION      BG924298
VERSION      BG924298.1 GI:14318821
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 631)
Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
Lark,M.W.
Identification and initial characterization of 5000 expressed
sequenced tags (ESTs) each from adult human normal and
osteoarthritic cartilage cDNA libraries
Osteoarthritis Cartilage 9 (7), 641-653 (2001)
21482651
Contact: Sanjay Kumar
DW2109
GlaxoSmithKline
709 Swedeiland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
Tel: 610-270-7245
Fax: 610-270-5598
Email: sanjay_kumar-1@gsk.com
Seq primer: T7.
FEATURES             source
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Best Local Similarity 99.6%; Pred. No. 5.6e-65;
Matches 544; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 86 ATCAGAGAAAACAGAACTAAGAAGTTGTGTAGATAGACTTCTTTTGTCTGTGACTGT 145

QY 6777 aaaaatcattttagagccactaataaccaatatttatttataaaaataaattcttaa 6836
Db 146 AAAAAATCATTTATGAGGCCACTAATAACCCAATATTTATTATTAGAAAAATAATCTTAA 205

QY 6837 ggcaagcgctatggctattttaagtgacttaaaagacagtcagggtcaaatgtattttg 6896
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QY 6897 catatgtcaacagatctttatctgtgtttgaaatgtatgcctgtaaaactaaaatccta 6956
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QY 7077 actatcttctgtactcttctgacttcatcattcggtcactcgtgcataaactcctgaagctt 7136
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Qy	7197	gatttgcacaaataactctgggaacaagctcttggcttgcggtccatgatgcaaaagaag	7256
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KEYWORDS	EST		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1. (bases 1 to 810)		
JOURNAL	Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.		
COMMENT	HRI human cDNA project Unpublished (2000) Contact: Takao Isogai Genomics Laboratory Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3951 Fax: 81-438-52-3952 Email: genomics@hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.		
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Qy	7093	ctcgtatttcattcatcctgctccgctcccaatcctgaagcttttgctgctcgctatt	7152
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Db 238 GATTTTCAGTCTCTTTGTGGCAATGGCCACACATTATGATATTTCCGATTTGCCAAATAC 297
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Db 478 GTTTTACCACAGCTGCTGCTTGAGAACTAAAGCTGTTTAGGAAACCTAAAGTCACGAGA 537
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Db 538 AATTAACGATTAAATTCCTTATGTTGAGGCATGGAAAAAAA 581

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ACCESSION AL550578
VERSION AL550578.1 GI:12887677
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 896)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Pollayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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BASE COUNT 265 a 155 c 165 g 310 t 1 others
ORIGIN
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Best Local Similarity 99.4%; Pred No. 1e-61;
Matches 521; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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ACCESSION AL550578
VERSION AL550578.1 GI:10995169
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 771)
AUTHORS Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3951
Fax: 81-438-52-3952
Email: genomics@hri.co.jp
HRI human cDNA project: 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
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BASE COUNT 225 a 142 c 155 g 243 t 6 others
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	AUTHORS	Li,W.B., Gruber,C., Jesse,J. and Polayes,D.
	TITLE	Full-length cDNA libraries and normalization
	JOURNAL	Unpublished (2001)
	COMMENT	Contact: Genoscope Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
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VERSION BG618204.1 GI:13669575			
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Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
REFERENCE 1 (bases 1 to 727)			
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.			
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL Unpublished (1999)			
COMMENT Contact: Robert Strausberg, Ph.D. Email: rgs@nih.gov Tissue Procurement: CLONTECH Laboratories, Inc. cDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLCMI629 row: h column: 07 High quality sequence stop: 724.			
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5'-ATTCTAGAGCCGAGCGCGGCACATG-dtt(30)BN-3' (where B = A,			
C, or G and N = A, C, G, or T). Average insert size 1.85			
kb (range 1.0-4.0 kb). 15/15 colonies contained inserts			
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VERSION AV704855.1 GI:10722167
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SOURCE human.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 731)
Peng, Y., Song, H., Huang, Q., Huang, C., Gu, Y., Yang, Y., Gao, G., Xiao
, H., Xu, X., Li, N., Qian, B., Liu, F., Qu, J., Gao, X., Cheng, Z., Xu, Z.,
Zeng, L., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu
, G., Hu, R., Chen, J., Chen, Z. and Han, Z.
Homo sapiens cDNA ADB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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FEATURES

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